

Research Article

Prevalence of Plasmid-Mediated Quinolone Resistance Determinants and OqxAB Efflux Pumps among Extended-Spectrum β -Lactamase Producing *Klebsiella pneumoniae* Isolated from Patients with Nosocomial Urinary Tract Infection in Tehran, Iran

Mehdi Goudarzi,^{1,2} Mehdi Azad,³ and Sima Sadat Seyedjavadi⁴

¹Infectious Diseases and Tropical Medicine Research Center, Shahid Beheshti University of Medical Sciences, Tehran 1985717443, Iran

²Department of Microbiology, School of Medicine, Shahid Beheshti University of Medical Sciences, Tehran 1985717443, Iran

³Department of Medical Laboratory Sciences, Faculty of Allied Medicine, Qazvin University of Medical Sciences, Qazvin 1651135779, Iran

⁴Department of Medical Mycology, Pasteur Institute of Iran, Tehran 1316943551, Iran

Correspondence should be addressed to Sima Sadat Seyedjavadi; sima_seyedjavadi@yahoo.com

Received 3 June 2015; Accepted 21 July 2015

Academic Editor: Joaquim Ruiz

Copyright © 2015 Mehdi Goudarzi et al. This is an open access article distributed under the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Objective. Plasmid-mediated quinolone resistance (PMQR) plays an important role in the development of clinical resistance to quinolone. The aim of this study was to investigate PMQR determinants among extended-spectrum β -lactamases- (ESBL-) producing *Klebsiella pneumoniae* recovered from patients with nosocomial urinary tract infection (UTI). **Methods.** A total of 247 ESBL-producing *K. pneumoniae* isolates were collected from 750 patients with UTI. ESBL production was confirmed by double disc synergy test and combined disc diffusion test. The prevalence of PMQR determinants among ESBL-producing *K. pneumoniae* was assessed using PCR method. **Results.** The rates of resistance to antimicrobial agents in present study varied from 14.2% to 98.8%. In comparison with other PMQR genotypes, the frequency of *aac(6')-Ib* (68.8%) was strikingly high. Of the 247 isolates tested, *qnrA*, *qnrB*, *qnrS*, and *qepA* genes were present in 3.6%, 1.6%, 1.2, and 2%, respectively. *oqxA* and *oqxB* were detected in 56.7% and 54.6% of isolates. The predominant coexisting ESBL and PMQR profile among our isolates included *bla*_{CTX-M} and *aac(6')-Ib*, *oqxA*, *oqxB* (28.3%) and *bla*_{TEM}, *bla*_{SHV} and *aac(6')-Ib*, *oqxA*, and *oqxB* (19.4%) profile. **Conclusion.** Given the linkage observed between resistance to quinolones and beta lactam antibiotics, therapeutic protocol with fluoroquinolones and beta lactam antibiotics should be seriously revised in Tehran hospitals.

1. Introduction

K. pneumoniae is common nosocomial pathogen causing urinary tract infection in different wards of hospital including infectious, surgical, and intensive care unit. During the last decade transferable multidrug resistance in Gram-negative bacteria, particularly *K. pneumoniae* isolates, has become an escalating global threat [1]. Beta lactam resistance is mediated

by acquisition of β -lactamase genes that are mostly plasmid encoded. Based on several investigators idea, plasmid-encoded temoneira (TEM), sulfhydryl variable (SHV), and cefotaximase (CTX-M) are the most prevalent ESBLs [2, 3].

Quinolone resistance among *K. pneumoniae* clinical isolates became a serious problem in developing countries as well as in developed countries, since the quinolones as broad-spectrum antimicrobial agents are widely prescribed for